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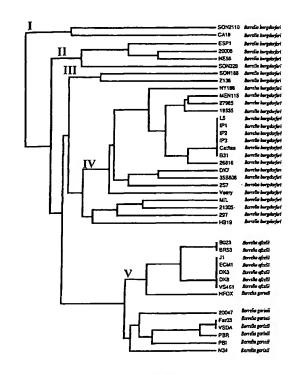
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(54) Title: A HIGH RESOLUTION TYPING SYSTEM FOR PATHOGENIC BORRELIA



VNTR Allelic Differences 0 (57) Abstract: MLVA methods for strain discrimination among globally diverseBorrelia isolates including B. burgdorferi, B. afzelii, and B. garinii are disclosed. Ten VNTR loci have been identified from genomic and plasmid sequences of Borreliastrains and primer pairs suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. The resolution of 30 unique genotypes into five to seven distinct groups is demonstrated.. This sub-typing scheme is useful for the epidemiological study of Borrelia and may be applied to the local detection of the pathological causative agent of Lyme Disease.



ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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